



EXHIBIT "B"

Home	Paracel BLAST Results	Help
------	-----------------------	------

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.

Database: human_genome

643 sequences; 200,654,690,654 total letters

Query= LEX 129 SEQ ID NO:1
(3648 letters)

	Score (bits)	E Value
Sequences producing significant alignments:		
chr10.25000001-30000000	2981	0.0
>chr10.25000001-30000000		
Length = 4999999		

Score = 2981 bits (1504), Expect = 0.0
Identities = 1504/1504 (100%)
Strand = Plus / Plus

Query: 2145 ggacgagctgaaaaaactctatgcccaactggaaatatataaaagaaagaagatgatcac 2204
|||||
Sbjct: 1036939 ggacgagctgaaaaaactctatgcccaactggaaatatataaaagaaagaagatgatcac
1036998

Query: 2205 aaacaacccccacctccagaaaaagcgggtgctcgaagaagggcctaggtcgttccatcat 2264
|||||
Sbjct: 1036999 aaacaacccccacctccagaaaaagcgggtgctcgaagaagggcctaggtcgttccatcat
1037058

Query: 2265 gagacgcattacggagatcccagagacagtcagccggcagtgctctaaagaggacaagga 2324
|||||
Sbjct: 1037059 gagacgcattacggagatcccagagacagtcagccggcagtgctctaaagaggacaagga
1037118

Query: 2325 gggcgccgaccatggcacagccaaaggcactgccctcatcaggaagaacccccagagtc 2384
|||||
Sbjct: 1037119 gggcgccgaccatggcacagccaaaggcactgccctcatcaggaagaacccccagagtc
1037178

Query: 2385 ttcaggaacacagggaaatccaaggaggagaccctgaaaaaccgagtccttctcactcaa 2444
|||||
Sbjct: 1037179 ttcaggaacacagggaaatccaaggaggagaccctgaaaaaccgagtccttctcactcaa
1037238

Query: 2445 gaaatccacagcacttatgaccacgtgagagaccaaacggaagagtccagtagcctacc 2504
|||||
Sbjct: 1037239 gaaatccacagcacttatgaccacgtgagagaccaaacggaagagtccagtagcctacc
1037298

Query: 2505 cacagaaagccaagaggaggagacaacagaaaattccacactggaatccctgtcgggtaa 2564
|||||
Sbjct: 1037299 cacagaaagccaagaggaggagacaacagaaaattccacactggaatccctgtcgggtaa
1037358

Query: 2565 aaaactaacacaaaaactaaaagaagacagcgaggctgagtcacaggagtcggtgccgtt 2624
|||||
Sbjct: 1037359 aaaactaacacaaaaactaaaagaagacagcgaggctgagtcacaggagtcggtgccgtt
1037418

Query: 2625 ggtgtgcaagtcagcaagcgctcacaacctcagctcagagaagaaaactgggcacccacg 2684
|||||
Sbjct: 1037419 ggtgtgcaagtcagcaagcgctcacaacctcagctcagagaagaaaactgggcacccacg
1037478

Query: 2685 aacatcgatgttacagaagtcctctcagtgctatagcaagcgccaaggagaagactcttgg 2744
|||||
Sbjct: 1037479 aacatcgatgttacagaagtcctctcagtgctatagcaagcgccaaggagaagactcttgg
1037538

Query: 2745 attagctgggaaaacccaaacagcaggtgtggaagaacgcactaaatcccagaaaccttt 2804
|||||
Sbjct: 1037539 attagctgggaaaacccaaacagcaggtgtggaagaacgcactaaatcccagaaaccttt
1037598

Query: 2805 gccaaaagataaagagacaaacagaaatcactcaaattctgataacacagagactaaaga 2864
|||||
Sbjct: 1037599 gccaaaagataaagagacaaacagaaatcactcaaattctgataacacagagactaaaga
1037658

Query: 2865 tcctgccccccaaaactcaaattctgcggaggagccaagaaagcctcagaaatctgggat 2924
|||||
Sbjct: 1037659 tcctgccccccaaaactcaaattctgcggaggagccaagaaagcctcagaaatctgggat
1037718

Query: 2925 tatgaaacaacaaaggggtcaaccccaccactgccaatctgacctgaacccaggcaccac 2984
|||||
Sbjct: 1037719 tatgaaacaacaaaggggtcaaccccaccactgccaatctgacctgaacccaggcaccac
1037778

Query: 2985 ccagatgaaggacaactttgacattggggagggtgtgtccttgggaggtttatgacctgac 3044

|||||
Sbjct: 1037779 ccagatgaaggacaactttgacattggggaggtgtgtccttgggaggttatgacctgac
1037838

Query: 3045 ccctggtcctgtgccttcagaatcaaaagttcaaaagcacgtatctattgtggcttctga 3104
|||||
Sbjct: 1037839 ccctggtcctgtgccttcagaatcaaaagttcaaaagcacgtatctattgtggcttctga
1037898

Query: 3105 aatggagaaaaacccactttttccttaaaggagaaatctcaccacaagcctaaggcagc 3164
|||||
Sbjct: 1037899 aatggagaaaaacccactttttccttaaaggagaaatctcaccacaagcctaaggcagc
1037958

Query: 3165 tgaggtttgtcagcaatccaatcagaagcgcatagataaggctgaagtatgcctttggga 3224
|||||
Sbjct: 1037959 tgaggtttgtcagcaatccaatcagaagcgcatagataaggctgaagtatgcctttggga
1038018

Query: 3225 gagccaaggccagtcatttttgaagatgagaagcttttgatttccaagactccagttct 3284
|||||
Sbjct: 1038019 gagccaaggccagtcatttttgaagatgagaagcttttgatttccaagactccagttct
1038078

Query: 3285 cccagagagggcaaaagaggagaacggaggtcagcctcgtgcagccaatgtgtgtgctgg 3344
|||||
Sbjct: 1038079 cccagagagggcaaaagaggagaacggaggtcagcctcgtgcagccaatgtgtgtgctgg
1038138

Query: 3345 gcagagcgaagaactgcccccaagctgtagcatcaaaaacagagaatgaaaatctcaa 3404
|||||
Sbjct: 1038139 gcagagcgaagaactgcccccaagctgtagcatcaaaaacagagaatgaaaatctcaa
1038198

Query: 3405 ccaaataggacaccaggaaaaaaagacatcttcttctgaggagaatgtgcgtggctccta 3464
|||||
Sbjct: 1038199 ccaaataggacaccaggaaaaaaagacatcttcttctgaggagaatgtgcgtggctccta
1038258

Query: 3465 taactcaagtaataacttcagcaacctttaacatcacgagcagaggtttgtccttggga 3524
|||||
Sbjct: 1038259 taactcaagtaataacttcagcaacctttaacatcacgagcagaggtttgtccttggga
1038318

Query: 3525 gtttgagaccccagctcaaccaaagtctggaagaagtgtagctttacctgcctcttctgc 3584
|||||
Sbjct: 1038319 gtttgagaccccagctcaaccaaagtctggaagaagtgtagctttacctgcctcttctgc
1038378

Query: 3585 tctaagtgc aaataagatagcagggcctaggaagaagagatctgggatagttttaagt 3644
|||||
Sbjct: 1038379 tctaagtgc aaataagatagcagggcctaggaagaagagatctgggatagttttaagt
1038438

Query: 3645 gtag 3648
||||
Sbjct: 1038439 gtag 1038442

Score = 1790 bits (903), Expect = 0.0
Identities = 903/903 (100%)
Strand = Plus / Plus

Query: 1 atgggagccatggcttacccttactcctctgcctcctgcttgctcagctgggattggga 60
|||||
Sbjct: 614589 atgggagccatggcttacccttactcctctgcctcctgcttgctcagctgggattggga 614648

Query: 61 gctgttggcgccagccgcgaccccccaaggacggccggattcccctcgagagaggacccccg 120
|||||
Sbjct: 614649 gctgttggcgccagccgcgaccccccaaggacggccggattcccctcgagagaggacccccg 614708

Query: 121 aaggggaagccgcacgcccagcagccgggtcgagcctctgcctcggactcctcgggtccc 180
|||||
Sbjct: 614709 aaggggaagccgcacgcccagcagccgggtcgagcctctgcctcggactcctcgggtccc 614768

Query: 181 tggagccgctccaccgatggcaccatcttggcgagaaactcgccgaggaggtgcccattg 240
|||||
Sbjct: 614769 tggagccgctccaccgatggcaccatcttggcgagaaactcgccgaggaggtgcccattg 614828

Query: 241 gacgtggcctcttacctctacaccggggactcccaccagctgaagcgagccaactgctcc 300
|||||
Sbjct: 614829 gacgtggcctcttacctctacaccggggactcccaccagctgaagcgagccaactgctcc 614888

Query: 301 ggccgctacgagttggcggggcctgccggggaagtggccagccctggccagcgcgacccc 360
|||||
Sbjct: 614889 ggccgctacgagttggcggggcctgccggggaagtggccagccctggccagcgcgacccc 614948

Query: 361 tccttgacccgggcgctggacacactgacacacgccaccaacttcctcaacgtgatgctg 420
|||||
Sbjct: 614949 tccttgacccgggcgctggacacactgacacacgccaccaacttcctcaacgtgatgctg 615008

Query: 421 cagagcaataagtcgcggggagcagaacttgaggacgacctggattggtaccaggcgctg 480
|||||
Sbjct: 615009 cagagcaataagtcgcggggagcagaacttgaggacgacctggattggtaccaggcgctg 615068

Query: 481 gtgtggagccttctggagggcgagcccagcatctcccgggcgcccatcaccttcagcacc 540
|||||
Sbjct: 615069 gtgtggagccttctggagggcgagcccagcatctcccgggcgcccatcaccttcagcacc 615128

Query: 541 gattcgctgtccgcaccggcccccacaggtcttctccaggccacgcgcgaggagagccgc 600
|||||
Sbjct: 615129 gattcgctgtccgcaccggcccccacaggtcttctccaggccacgcgcgaggagagccgc 615188

Query: 601 atcctgctccaagacctgtcctcctccgcacccacactggccaacgccactctggagacc 660
|||||
Sbjct: 615189 atcctgctccaagacctgtcctcctccgcacccacactggccaacgccactctggagacc 615248

Query: 661 gagtggttccacggcctccggcgcaagtggaggccccacttacaccgcccggccccaat 720
|||||
Sbjct: 615249 gagtggttccacggcctccggcgcaagtggaggccccacttacaccgcccggccccaat 615308

Query: 721 caggggccccggggcctggggccacagctggcggcgcaaggacgggctcggcggggacaag 780
|||||
Sbjct: 615309 caggggccccggggcctggggccacagctggcggcgcaaggacgggctcggcggggacaag 615368

Query: 781 agccacttcaagtgggtctccgccttatctggagtgcgagaacgggagttacaagcccgga 840
|||||
Sbjct: 615369 agccacttcaagtgggtctccgccttatctggagtgcgagaacgggagttacaagcccgga 615428

Query: 841 tggctgggttactctttcctctgcatctacgggttgacgcctaacctgggtcccgggaattc 900
|||||
Sbjct: 615429 tggctgggttactctttcctctgcatctacgggttgacgcctaacctgggtcccgggaattc 615488

Query: 901 agg 903
|||
Sbjct: 615489 agg 615491

Score = 478 bits (241), Expect = e-131
Identities = 241/241 (100%)
Strand = Plus / Plus

Query: 1513 aggggttttgaaggtgtttctttcacgaacgggtcaacgaattccatatatgactggcgga 1572
|||||
Sbjct: 1011815 aggggttttgaaggtgtttctttcacgaacgggtcaacgaattccatatatgactggcgga
1011874

Query: 1573 cgggtcatgaggatgctggcagtaatactcttggtagtgttttggtttctcattggctgg 1632
|||||

Sbjct: 1011875 cgggtcatgaggatgctggcagtaataactcttggtagtggtttgggtttctcattggctgg
1011934

Query: 1633 acttcatctgtgtgccagaatttggagaaacagatttcacttattggccaggggaaaaca 1692
|||||
Sbjct: 1011935 acttcatctgtgtgccagaatttggagaaacagatttcacttattggccaggggaaaaca
1011994

Query: 1693 tccgatcacctcatcttcaatatgtgcctcattgaccgctgggactacatgacagcagtt 1752
|||||
Sbjct: 1011995 tccgatcacctcatcttcaatatgtgcctcattgaccgctgggactacatgacagcagtt
1012054

Query: 1753 g 1753
|
Sbjct: 1012055 g 1012055

Score = 438 bits (221), Expect = e-119
Identities = 231/234 (98%), Gaps = 1/234 (0%)
Strand = Plus / Plus

Query: 1102 aactttcggagaaggggtccggatcagcatatttcaggaagtacaaaagatgtgtcagaa 1161
|||||
Sbjct: 851409 aactttcag-gaaggggtccggatcagcatatttcaggaagtacaaaagatgtgtcagaa 851467

Query: 1162 gaagcctatgtctgcctaccttgcagggagggctgccccttctgtgctgatgacagccca 1221
|||||
Sbjct: 851468 gaagcctatgtctgcctaccttgcagggagggctgccccttctgtgctgatgacagccca 851527

Query: 1222 tgcttcgtccaggaagataagtatattacgacttgccatcatctccttccaaggcctgtgt 1281
|||||
Sbjct: 851528 tgcttcgtccaggaagataagtatattacgacttgccatcatctccttccaaggcctgtgt 851587

Query: 1282 atgctgctcgacttcgtttagcatgctgggtggtctaccactttcgcaaagcaaag 1335
|||||
Sbjct: 851588 atgctgctcgacttcgtttagcatgctgggtggtctaccactttcgcaaagcaaag 851641

Score = 297 bits (150), Expect = 2e-77
Identities = 150/150 (100%)
Strand = Plus / Plus

Query: 1997 agttttcacattcaagcaataaaccacgagatgatattgctacagaagcatatgaggatg 2056
|||||
Sbjct: 1035809 agttttcacattcaagcaataaaccacgagatgatattgctacagaagcatatgaggatg
1035868

Query: 2057 agctagacatgggccgatctggatcctacctgaacagcagtatcaattcagcctggagtg 2116
|||||
Sbjct: 1035869 agctagacatgggccgatctggatcctacctgaacagcagtatcaattcagcctggagtg
1035928

Query: 2117 agcacagcttggatccagaggacattcggg 2146
|||||
Sbjct: 1035929 agcacagcttggatccagaggacattcggg 1035958

Score = 278 bits (140), Expect = 2e-71
Identities = 140/140 (100%)
Strand = Plus / Plus

Query: 1753 gctgaatttttattcctcttgtggggtgtttatctctgctatgcagtgcggaacagtccca 1812
|||||
Sbjct: 1028174 gctgaatttttattcctcttgtggggtgtttatctctgctatgcagtgcggaacagtccca
1028233

Query: 1813 tcggcattccatgagccccgctatatggctgttgagttcacaatgagctcatcatctct 1872
|||||
Sbjct: 1028234 tcggcattccatgagccccgctatatggctgttgagttcacaatgagctcatcatctct
1028293

Query: 1873 gctatattccatacaattag 1892
|||||
Sbjct: 1028294 gctatattccatacaattag 1028313

Score = 220 bits (111), Expect = 5e-54
Identities = 111/111 (100%)
Strand = Plus / Plus

Query: 1405 gttgttattttgtactttgagccaagcacatttcgctgtattctcctaagatgggctcgt 1464
|||||
Sbjct: 990144 gttgttattttgtactttgagccaagcacatttcgctgtattctcctaagatgggctcgt 990203

Query: 1465 cttctcgggttttgcactgtttacggaactgtcactctcaaacttcacagg 1515
|||||
Sbjct: 990204 cttctcgggttttgcactgtttacggaactgtcactctcaaacttcacagg 990254

Score = 214 bits (108), Expect = 3e-52
Identities = 108/108 (100%)
Strand = Plus / Plus

Query: 901 aggggtgtcatgaaagttgacataaatcttcagaaagtggaacattgaccaatgctcaagt 960
|||||
Sbjct: 660218 aggggtgtcatgaaagttgacataaatcttcagaaagtggaacattgaccaatgctcaagt 660277

Query: 961 gatggctgggttttcaggaactcataaatgccacctcaacaattcagag 1008
|||||
Sbjct: 660278 gatggctgggttttcaggaactcataaatgccacctcaacaattcagag 660325

Score = 214 bits (108), Expect = 3e-52
Identities = 108/108 (100%)
Strand = Plus / Plus

Query: 1891 agatttgttcttgccctcaagacttcagtctgattggatggtgatgctgtattttgcacat 1950
|||||
Sbjct: 1033458 agatttgttcttgccctcaagacttcagtctgattggatggtgatgctgtattttgcacat
1033517

Query: 1951 actcatttgactgtgacagtcaccattgggttgcttttgattccaaag 1998
|||||
Sbjct: 1033518 actcatttgactgtgacagtcaccattgggttgcttttgattccaaag 1033565

Score = 212 bits (107), Expect = 1e-51
Identities = 110/111 (99%)
Strand = Plus / Plus

Query: 1002 ttcagagtgtatgccaatataaggcctaggattcggttcttgaggcctatgagtgcatttg 1061
|||||
Sbjct: 835072 ttcagagtgtatgccaatataaggcctaggattcggttcttgaggcctatgagtgcatttg 835131

Query: 1062 caaagcaggattctatcatcctggagtcttaccagtgaacaactttcggag 1112
|||||
Sbjct: 835132 caaagcaggattctatcatcctggagtcttaccagtgaacaactttcggag 835182

Score = 145 bits (73), Expect = 2e-31
Identities = 73/73 (100%)
Strand = Plus / Plus

Query: 1334 agagcatccgggcatcgggccttatcctggttgaaacgatcctttttggatctctgctcc 1393
|||||
Sbjct: 905817 agagcatccgggcatcgggccttatcctggttgaaacgatcctttttggatctctgctcc 905876

Query: 1394 tatactttccagt 1406
|||||

Sbjct: 905877 tatactttccagt 905889

Database: mouse_genome

Posted date: Jul 30, 2003 8:10 AM

Number of letters in database: 200,654,690,654

Number of sequences in database: 643

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 0, Extension: 0

Number of Hits to DB: 0

length of query: 7298

length of database: 200,654,690,654

effective HSP length: 22

effective length of query: 3626

effective search space used: 0

T: 0

A: 0

X1: 0 (0.0 bits)

X2: 20 (39.6 bits)

S1: 12 (24.3 bits)

S2: 24 (48.1 bits)